PCT09

RAW SEQUENCE LISTING   DATE: 08/01/2001
PATENT APPLICATION: US/09/719,088A   TIME: 14:21:53

        Input Set : A:\92979.txt
        Output Set: N:\CRF3\08012001\I719088A.raw

        4 <110> APPLICANT: Garvan Institute of Medical Research   ENTERED
        6 <120> TITLE OF INVENTION: NPY-Y7 Receptor Gene
W--> 0 <130> FILE REFERENCE:
C--> 8 <140> CURRENT APPLICATION NUMBER: US/09/719,088A
C--> 9 <141> CURRENT FILING DATE: 2001-05-09
       11 <150> PRIOR APPLICATION NUMBER: PP 4385
       12 <151> PRIOR FILING DATE: 1998-06-29
       14 <160> NUMBER OF SEQ ID NOS: 5
       16 <170> SOFTWARE: PatentIn Ver. 2.1
       18 <210> SEQ ID NO: 1
       19 <211> LENGTH: 14
       20 <212> TYPE: PRT
       21 <213> ORGANISM: Artificial Sequence
       23 <220> FEATURE:
       24 <223> OTHER INFORMATION: Description of Artificial Sequence: N-terminal
       25   consensus sequence
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W--> 28 <221> NAME/KEY: misc-feature
       29 <222> LOCATION: (2)/.(3)..(5)..(10)
       30 <223> OTHER INFORMATION: Xaa = any codable amino acid
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       38 <211> LENGTH: 408
       39 <212> TYPE: PRT
       40 <213> ORGANISM: Homo sapiens
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       46 His Pro Ile Trp Asn Val Asn Asp Thr Lys His His Leu Tyr Ser Asp
       47   20   25   30
       49 Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala
       50   35   40   45
       52 Ala Ile Phe Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met
       53   50   55   60
       55 Gly Asn Thr Val Val Cys Phe Ile Val Met Arg Asn Lys His Met His
       56   65   70   75   80
       58 Thr Val Thr Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu
       59   85   90   95
       61 Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala
       62   100   105   110
       64 Gly Trp Pro Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu Val Gln
       65   115   120   125
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       68   130   135   140
       70 Asp Arg Phe Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile

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71 145                    150                    155                    160
73 Lys Thr Ala Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala Ile Thr
74               165                    170                    175
76 Ile Met Ser Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr
77          180                    185                    190
79 Tyr Arg Val Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp
80          195                    200                    205
82 Cys Arg Glu Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr
83      210                    215                    220
85 Val Leu Phe Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile
86 225                    230                    235                    240
88 Met Tyr Gly Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His
89               245                    250                    255
91 Thr Gly Arg Lys Asn Gln Glu Gln Trp His Val Val Ser Arg Lys Lys
92          260                    265                    270
94 Gln Lys Ile Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe Ile Leu
95          275                    280                    285
97 Ser Trp Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp
98      290                    295                    300
100 Leu Ser Pro Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe
101 305                    310                    315                    320
103 Ala His Trp Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr
104               325                    330                    335
106 Gly Phe Phe Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln
107          340                    345                    350
109 Leu Gln Leu Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Thr Leu
110          355                    360                    365
112 Lys Ala Lys Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln
113      370                    375                    380
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131 Asn His Ile Trp Ser Gly Asn Asp Thr Gln His His Trp Tyr Ser Asp
132          20                    25                    30
134 Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala
135          35                    40                    45
137 Ala Val Phe Ile Ser Ser Tyr Leu Leu Ile Phe Val Leu Cys Met Val
138      50                    55                    60
140 Gly Asn Thr Val Val Cys Phe Ile Val Ile Arg Asn Arg His Met His
141 65                    70                    75                    80
143 Thr Val Thr Asn Phe Leu Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu
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144                 85              90              95
146 Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala
147             100             105             110
149 Gly Trp Pro Phe Gly Ser Ser Met Cys Lys Ile Ser Gly Leu Val Gln
150         115             120             125
152 Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val
153     130             135             140
155 Asp Arg Phe Arg Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Val
156 145             150             155             160
158 Lys Thr Ala Phe Val Thr Ile Val Ile Ile Trp Gly Leu Ala Ile Ala
159             165             170             175
161 Ile Met Thr Pro Ser Ala Ile Met Leu His Val Gln Glu Glu Lys Tyr
162         180             185             190
164 Tyr Arg Val Arg Leu Ser Ser His Asn Lys Thr Ser Thr Val Tyr Trp
165     195             200             205
167 Cys Arg Glu Asp Trp Pro Arg His Glu Met Arg Arg Ile Tyr Thr Thr
168     210             215             220
170 Val Leu Phe Ala Ile Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile
171 225             230             235             240
173 Met Tyr Ala Arg Ile Gly Ala Ser Leu Phe Lys Thr Ala Ala His Cys
174             245             250             255
176 Thr Gly Lys Gln Arg Pro Val Gln Cys Met Tyr Gln Glu Lys Gln Lys
177         260             265             270
179 Val Ile Lys Met Leu Leu Thr Val Ala Leu Leu Phe Ile Leu Ser Trp
180         275             280             285
182 Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Thr Asp Leu Ser
183     290             295             300
185 Pro Asn Lys Leu Arg Ile Ile Asn Ile Tyr Ile Tyr Pro Phe Ala His
186 305             310             315             320
188 Trp Leu Ala Phe Cys Asn Ser Ser Val Asn Pro Ile Ile Tyr Gly Phe
189             325             330             335
191 Phe Asn Glu Asn Phe Arg Asn Gly Phe Gln Asp Ala Phe Gln Ile Cys
192         340             345             350
194 Gln Lys Lys Ala Lys Pro Gln Glu Ala Tyr Ser Leu Arg Ala Lys Arg
195         355             360             365
197 Asn Ile Val Ile Asn Thr Ser Gly Leu Leu Val Gln Glu Pro Val Ser
198     370             375             380
200 Gln Asn Pro Gly Gly Glu Asn Leu Gly Cys Gly Lys Ser Ala Asp Asn
201 385             390             395             400
203 Pro His Arg Asn Pro
204                 405
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208 <211> LENGTH: 1903
209 <212> TYPE: DNA
210 <213> ORGANISM: Homo sapiens
212 <400> SEQUENCE: 4
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214 cacgcctggc taattttttt gtattttttag tagggacggc gtttcactgt gttagccaga 120
215 tggtctccat ctcccgacct cgtgatccac ccacctcggc ctcccaaagt gctgggatta 180
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216 caggcgtgag accgcgcccg gccaatttcc tttcttagtt gcctctgccc acctcttctc 240
217 ttctgcttcc atattacagg tttcctcagt tgcgaaatta ggatgttaat tatagctttt 300
218 gacatacaag aaacatcaaa aagattgaat gtcttaataa gagtgaagca tgtagatcag 360
219 tgactgctat gttcatcatg aatgagaaat gggacacaaa ctcttcagaa aactggcatc 420
220 ccatctggaa tgtcaatgac acaaagcatc atctgtactc agatattaat attacctatg 480
221 tgaactacta tcttcaccag cctcaagtgg cagcaatctt cattatttcc tactttctga 540
222 tcttcttttt gtgcatgatg ggaaatactg tggtttgctt tattgtaatg aggaacaaac 600
223 atatgcacac agtcactaat ctcttcatct taaacctggc cataagtgat ttactagttg 660
224 gcatattctg catgcctata acactgctgg acaatattat agcaggatgg ccatttggaa 720
225 acacgatgtg caagatcagt ggattggtcc aggaatatc tgtcgcagct tcagtcttta 780
226 cgttagttgc aattgctgta gataggttcc agtgtgtggt ctaccctttt aaaccaaagc 840
227 tcactatcaa gacagcgttt gtcattatta tgatcatctg ggtcctagcc atcaccatta 900
228 tgtctccatc tgcagtaatg ttacatgtgc aagaagaaaa atattaccga gtgagactca 960
229 actcccagaa taaaaccagt ccagtctact ggtgccggga agactggcca aatcaggaaa 1020
230 tgaggaagat ctacaccact gtgctgtttg ccaacatcta cctggctccc ctctccctca 1080
231 ttgtcatcat gtatggaagg attggaattt cactcttcag ggctgcagtt cctcacacag 1140
232 gcaggaagaa ccaggagcag tggcacgtgg tgtccaggaa gaagcagaag atcattaaga 1200
233 tgctcctgat tgtggccctg cttttttattc tctcatggct gcccctgtgg actctaatga 1260
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235 acccttttgc acactggctg gcattcggca acagcagtgt caatcccatc atttatggtt 1380
236 tcttcaacga gaatttccgc cgtggtttcc aagaagcttt ccagctccag ctctgccaaa 1440
237 aaagagcaaa gcctatggaa gcttataccc taaaagctaa aagccatgtg ctcataaaca 1500
238 catctaatca gcttgtccag gaatctacat ttcaaaaccc tcatggggaa accttgcttt 1560
239 ataggaaaag tgctgaaaac cccaacagga attagtgatg gaagaattaa aagaaactac 1620
240 taacagcagt gagatttaaa aagagctagt gtgataatcc taactctact acgcattata 1680
241 tatttaaatc cattgctttt tgtggctttg cacttcaaat ttttcaaaga atgttctaaa 1740
242 taaaacattt actgaaagcc ctctctggca aaaaaattaa aaataaacaa aaatggtcat 1800
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247 <211> LENGTH: 1228
248 <212> TYPE: DNA
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251 <400> SEQUENCE: 5
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254 tatctccacc agccccaagt ggcagctgtc ttcatcagct cctacctcct gatctttgtc 180
255 ttgtgcatgg tgggaaatac tgtcgtttgc tttattgtga taaggaatag acacatgcac 240
256 acagtcacta atttcttgat cttaaacctt gccataagtg atttactggt tggaatattc 300
257 tgtatgccta tcacattgct ggacaacatc atagcaggat ggccattcgg aagcagcatg 360
258 tgcaagatca gtgggctggt gcaaggata tcagttgcgg cttccgtctt caccttggtt 420
259 gcaatagctg tggacagatt ccgctgtgtg tctacccct ttaagccaaa gctcactgtc 480
260 aagacagcct ttgtcacgat tgtgatcatc tggggcctgg ccatcgccat tatgactcca 540
261 tctgcaataa tgttacatgt acaagaagaa aaatactacc gtgtgagact cagctcccac 600
262 aataaaacca gcacagtcta ctggtgtcgg gaggactggc caagacacga aatgaggagg 660
263 atctatacca cggtgctatt tgccatcatc tatcttgctc ctctctcact cattgttatc 720
264 atgtatgcaa ggattggggc ttccctcttc aagacggcag cacactgcac aggcaagcag 780
265 cgtccagtgc agtgcatgta tcaagagaaa cagaaggtca tcaagatgct gctgactgtg 840
266 gccctccttt tcatcctttc ctggcttccc ctgtggaccc tgatgatgct ctcagactat 900
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268 tggctcgcct tctgcaacag cagtgtcaac cctattattt atggattctt taatgaaaat 1020
269 tttcgcaatg gtttccaaga tgctttccag atctgccaaa agaaagccaa gccccaggaa 1080
270 gcctattccc tgagagcgaa acgcaacata gtcataaaca catcgggcct gctggtgcag 1140
271 gaaccggtgt ctcaaaaccc aggtggggaa aatttgggat gtggaaaaag tgcagacaat 1200
272 ccacacagga atccttgata gaggaatg                                    1228
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VERIFICATION SUMMARY   DATE: 08/01/2001
PATENT APPLICATION: US/09/719,088A   TIME: 14:21:54

Input Set : A:\92979.txt
Output Set: N:\CRF3\08012001\I719088A.raw

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L:8 M:270 C: Current Application Number differs, Replaced Current Application Number
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1